

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 25, 2003, 14:20:45 : Search time 5.40155 Seconds

(Without alignments)
798.574 Million cell updates/sec

Title: US-09-622-613B-11

Perfect score: 577
Sequence: 1 SDWLFEOKKHLTNTRPVDCN.....TFCVTCENQAPVHEVGVGHC 104

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt.40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	551	95.5	104 1	RN30_RANPI
2	287	49.7	111 1	RNPO_RANCA
3	280.5	48.6	111 1	LECS_RANJA
4	264.5	45.8	111 1	RNPL_RANCA
5	144	25.0	119 1	RNP_IGUIG
6	132	22.6	124 1	RNP_GALMU
7	130.5	22.6	145 1	ANGR_MOUSE
8	130.5	22.6	146 1	ANGI_CERAE
9	128	22.2	148 1	ANGI_BOVIN
10	126	21.8	128 1	RNP_MYOCO
11	125	21.7	124 1	RNP_BALAC
12	121.5	21.1	146 1	ANGI_MACMU
13	120	20.8	128 1	RNPB_CAVPO
14	120	20.8	128 1	RNP_PROGU
15	119.5	20.7	145 1	ANGI_MOUSE
16	118.5	20.5	146 1	ANGI_PAPAE
17	118	20.5	124 1	RNP_CHIBR
18	117	20.3	128 1	RNP_HYDHY
19	116	20.1	125 1	ANGI_RABIT
20	115	19.9	146 1	ANGI_MIORA
21	114	19.8	124 1	RNP_HIPAM
22	113	19.6	147 1	ANGI_HUMAN
23	113	19.6	147 1	ANGI_PANTR
24	113	19.6	156 1	ECP3_MOUSE
25	112	19.4	124 1	RNP_PIG
26	112	19.4	128 1	RNP_HYSCR
27	112	19.4	150 1	RNP_BOVIN
28	112	19.4	156 1	RNP_MYOGI
29	111.5	19.3	147 1	RNL4_HUMAN
30	111	19.2	128 1	RNP_HORSE
31	111	19.2	146 1	ANGI_SAISC
32	111	19.2	167 1	RNBR_BOVIN
33	110.5	19.2	123 1	ANGI_PIG

34	110.5	19.2	155 1	ECP1_MOUSE	P97426	mus musculus
35	110	19.1	124 1	RNPA_CAVPO	P00678	cavia porce
36	110	19.1	141 1	RNBR_GIRCA	Q29542	giraffa cam
37	110	19.1	146 1	ANGI_SAGOE	Q8W652	saquinus oe
38	110	19.1	151 1	RNBR_AXIPR	P87350	axis porcin
39	110	19.1	156 1	ECP2_MOUSE	P97425	mus musculus
40	109	18.9	123 1	ANG2_BOVIN	P80929	bos taurus
41	109	18.9	124 1	RNP_AEPMF	P07847	aepeyceros m
42	109	18.9	124 1	RNP_ANTAM	P00668	antilocapra
43	109	18.9	124 1	RNP_SHEEP	P00661	ovis aries
44	108.5	18.8	150 1	RNK6_SAISC	Q46528	salimiri sci
45	108.5	18.8	155 1	ECP_RAT	P70705	rattus norv

ALIGNMENTS

RESULT 1	ID	Sequence	STANDARD	PRT	104 AA.
RN30_RANPI					
AC	P22069:				
DT	01-AUG-1991 (Rel. 19, Created)				
DT	01-FEB-1994 (Rel. 28, Last, sequence update)				
DT	01-FEB-1995 (Rel. 31, Last annotation update)				
DE	P-30 protein (EC 3.1.27.-) (Onconase).				
OC	Rana pipiens (Northern leopard frog).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.				
OX	NCBI_TaxID=8404;				
RM	[1]				
RP	SEQUENCE.				
RP	TISSUE=Embryo;				
RC	Medline=91093131; Pubmed=1985896;				
RX	Ardelet W., Mikulski S.M., Shogen K.;				
RA	"Amino acid sequence of an anti-tumor protein from Rana pipiens oocytes and early embryos. Homology to pancreatic ribonucleases.";				
RT	J. Biol. Chem. 266:245-251(1991).				
RL	[2]				
RM	3D-STRUCTURE MODELING.				
RP	Medline=93066156; Pubmed=1438177;				
RX	Mostmann S.C., Johns K.L., Ardelet W., Mikulski S.M., Shogen K.,				
RA	James M.N.G.;				
RT	"Comparative molecular modeling and crystallization of P-30 protein: a novel antitumor protein of Rana pipiens oocytes and early embryos.";				
RL	Proteins 14:392-400(1992).				
RN	[3]				
RP	X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS).				
RX	Medline=94166079; Pubmed=8120892;				
RA	Mostmann S.C., Ardelet W., James M.N.G.;				
RT	"Refined 1.7 A X-ray crystallographic structure of P-30 protein, an amphibian ribonuclease with anti-tumor activity.";				
RL	J. Mol. Biol. 236:1141-1153(1994).				
CC	- FUNCTION: BASIC PROTEIN WITH ANTIPROLIFERATIVE/CYTOTOXIC ACTIVITY AGAINST SEVERAL TUMOR CELL LINES IN VITRO, AS WELL AS ANTITUMOR IN VIVO. IT EXHIBITS A RIBONUCLEASE-LIKE ACTIVITY AGAINST HIGH MOLECULAR WEIGHT RIBOSOMAL RNA.				
CC	- DEVELOPMENTAL STAGE: EARLY EMBRYOS (UP TO FOUR BLASTOMERE STAGE).				
CC	- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.				
DR	PDB: 1ONC; 31-JAN-94.				
DR	InterPro: IPR001427; RNaseA.				
DR	Pfam: PF00074; RNaseA; 1.				
DR	Prodom: PD000535; RNaseA; 1.				
DR	SMART: SM00092; RNase; PC: 1.				
DR	PROSITE: PS00127; RNASE_PANCREATIC; 1.				
KW	Hydrolase; Nuclease; Endonuclease; 3D-structure.				
FT	MOD_RES				
FT	ACT_SITE				
FT	ACT_SITE				
FT	ACT_SITE				
FT	DISULFID				
FT	DISULFID				
FT	DISULFID				

FT DISULFID 87 104
 FT HELIX 3 10
 FT STRAND 11 12
 FT HELIX 19 22
 FT TURN 23 24
 FT TURN 26 30
 FT STRAND 33 38
 FT HELIX 41 48
 FT TURN 49 50
 FT STRAND 55 58
 FT STRAND 63 70
 FT TURN 74 75
 FT STRAND 86 91
 FT STRAND 92 93
 FT TURN 94 101
 FT STRAND 104 AA: 11845 MW: 22A753C2P9E56B4 CRC64;

Query Match 95.5%; Score 551; DB 1; Length 104;
 Best Local Similarity 96.1%; Pred. No. 4.1e-52;
 Matches 99; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 DWLTFQKHLLTNTRDVCNNIMSTNLFHCKDKNTFIYSRPPVKAICGIIASKNVLTTS 61
 DB 2 DWLTFQKHLLTNTRDVCNNIMSTNLFHCKDKNTFIYSRPPVKAICGIIASKNVLTTS 61
 QY 62 EFTLSDCNVTSRPPCKYKLLKSTNFCVTCENQAPVHFVGVGHC 104
 DB 62 EFTLSDCNVTSRPPCKYKLLKSTNFCVTCENQAPVHFVGVGSC 104

RESULT 2
 RNPO_RANCA STANDARD: PRT: 111 AA.

ID RNPO_RANCA STANDARD: PRT: 111 AA.
 AC P11916;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Ribonuclease, oocytes (EC 3.1.27.-) (RC-RNase) (Stallic acid-binding
 lectin) (SRI-C).
 OS Rana catesbeiana (Bull. frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
 OX NCBI_TaxID=8400;
 RN [1]
 RP SEQUENCE.

RC TISSUE=Egg;
 RX MEDLINE=87299649; PubMed=3304421;
 RA Titani K., Takio K., Kuwada M., Nitta K., Sakakibara F., Kawauchi H.,
 RT Takayanagi G., Hakomori S.;
 RT "Amino acid sequence of stallic acid binding lectin from frog (Rana
 catesbeiana) eggs";
 RL Biochemistry 26:2189-2194(1987).
 RN [2]
 RP CHARACTERIZATION, AND SEQUENCE OF 59-79.
 RX MEDLINE=92220613; PubMed=1373237;
 RA Liao Y.-D.;
 RT "A pyrimidine-guanine sequence-specific ribonuclease from Rana
 catesbeiana (bullfrog) oocytes";
 RL Nucleic Acids Res. 20:1371-1377(1992).
 RN [3]
 RP CHARACTERIZATION.

RC TISSUE=Egg;
 RX MEDLINE=93192604; PubMed=8448385;
 RA Nitta K., Oyama F., Oyama R., Sekiguchi K., Kawauchi H.,
 RT Takayanagi Y., Hakomori S., Titani K.;
 RT "Ribonuclease activity of stallic acid-binding lectin from Rana
 catesbeiana eggs";
 RL Glycobiology 3:37-45(1993).
 RN [4]

RP STRUCTURE BY NMR.
 RX MEDLINE=98437383; PubMed=9761686;
 RA Chang C.-F., Chen C., Chen Y.-C., Hom K., Huang R.-F., Huang T. H.;

RT "The solution structure of a cytotoxic ribonuclease from the oocytes
 of Rana catesbeiana (bullfrog).";
 RL J. Mol. Biol. 283:231-244(1998).
 CC -1- FUNCTION: PREFERENTIALLY CLEAVES SINGLE-STRANDED RNA AT PYRIMIDINE
 RESIDUES WITH A 3'FLANKING GUANINE. HYDROLYSES POLY(U) AND POLY(C)
 AS SUBSTRATES, AND PREFERENCES THE FORMER. THE S-LECTINS IN FROG EGGS
 MAY BE INVOLVED IN THE FERTILIZATION AND DEVELOPMENT OF THE FROG
 EMBRYO. THIS LECTIN AGGLOUTINATES VARIOUS ANIMAL CELLS, INCLUDING
 NORMAL LYMPHOCYTES, ERYTHROCYTES, AND FIBROBLASTS OF ANIMAL AND
 HUMAN ORIGIN.
 CC -1- SUBUNIT: MONOMER.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
 DR PIR: A27121; A27121.
 DR PDB: 1BC4; 28-OCT-98.
 DR InterPro: IPR001427; RNaseA.
 DR Pfam: PF00074; RNaseA; 1.
 DR PRODOM: PD000535; RNaseA; 1.
 DR SMART: SM00092; RNase_Pc; 1.
 DR PROSITE: PS00127; RNASE_PANCREATIC; 1.
 KW Hydrolyase; Nuclease; Endonuclease; Stallic acid; Lectin; 3D-structure.
 FT MOD_RES 1 1
 FT ACT_SITE 10 10
 FT ACT_SITE 35 35
 FT ACT_SITE 103 103
 FT DISULFID 19 71
 FT DISULFID 34 81
 FT DISULFID 52 96
 FT DISULFID 93 110
 SQ SEQUENCE 111 AA: 12464 MW: 0BC9E5F5729ECF4 CRC64;

Query Match 49.7%; Score 287; DB 1; Length 111;
 Best Local Similarity 49.1%; Pred. No. 6e-24;
 Matches 54; Conservative 16; Mismatches 32; Indels 8; Gaps 3;

QY 2 DWLTFQKHLLTNTRDVCNNIMSTNLFHCKDKNTFIYSRPPVKAICGIIASKNV 57
 DB 2 DWLTFQKHLLTNTRDVCNNIMSTNLFHCKDKNTFIYSRPPVKAICGIIASKNV 57
 QY 58 LTTSEFLSDC---NVTSPCKYKLLKSTNFCVTCENQAPVHFVGVGHC 104
 DB 61 LSTTRQLNLTCTRTSTTPRCPYSSRTETNYICVNCENQAPVHFVGVGHC 110

RESULT 3
 LSCS_RANCA STANDARD: PRT: 111 AA.

ID LSCS_RANCA STANDARD: PRT: 111 AA.
 AC P18839;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Stallic acid-binding lectin (EC 3.1.27.-).
 OS Rana japonica (Japanese reddish frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
 OX NCBI_TaxID=8402;
 RN [1]
 RP SEQUENCE, AND DISULFIDE BONDS.

RC TISSUE=Egg;
 RX MEDLINE=91035319; PubMed=2229005;
 RA Kamaya Y., Oyama F., Oyama R., Sakakibara F., Nitta K., Kawauchi H.,
 RT Takayanagi Y., Titani K.;
 RT "Amino acid sequence of a lectin from Japanese frog (Rana japonica)
 eggs";
 RL J. Biochem. 108:139-143(1990).
 CC -1- FUNCTION: THE S-LECTINS IN FROG EGGS MAY BE INVOLVED IN THE
 FERTILIZATION AND DEVELOPMENT OF THE FROG EMBRYO. THIS LECTIN
 PREFERENTIALLY AGGLOUTINATE A LARGE VARIETY OF TUMOR CELLS, BUT IT
 DOES NOT AGGLOUTINATE NON-TRANSFORMED CELLS AND ERYTHROCYTES.

CC -1- SUBUNIT: MONOMER.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
 DR PIR: JX0120; JX0120.

RESULT 4			
ID	RNPL_RANCA	STANDARD;	PRT; 111 AA.
AC	P16626		
DT	01-APR-1990 (Rel; 14, Created)		
DT	01-FEB-1994 (Rel; 28, Last sequence update)		
DT	15-JUN-2002 (Rel; 41, Last annotation update)		
DE	Ribonuclease, liver (EC 3.1.27.5).		
OS	Rana catesbeiana (bull frog)		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.		
OX	NCBI_TaxID=9400;		
RA	[1]		
RP	SEQUENCE.		
RX	TISSUE=Liver;		
CC	MEDLINE=90130374; PubMed=2613682;		
CC	Nita R., Katayama N., Okabe Y., Iwama M., Watanabe H., Abe Y.,		
CC	Okazaki T., Ohgi K., Irie M.;		
CC	"Primary structure of a ribonuclease from bullfrog (<i>Rana catesbeiana</i>)		
CC	liver.";		
CC	J. Biochem. 106:729-735(1989).		
CC	-1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-p		
CC	phosphates and 3'-phosphooligonucleotides ending in C-P or U-P		
CC	with 2',3'-cyclic phosphate intermediates.		
CC	-1- SUBCELLULAR LOCATION: Secreted.		
CC	-1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.		
CC	PIR: JX0085; JX0085.		
DR	HSP: P11916; JBC4.		
DR	InterPro: IPR001427; RNaseA.		
DR	Pfam: PF00074; RNaseA: 1.		
DR	ProDom: PD000535; RNaseA: 1.		
DR	SMART: SM0092; RNase_PC: 1.		
DR	PROSITE: P500127; RNase_PANCREATIC: 1.		
KW	Hydrolase; Nuclease; Endonuclease.		
FT	MOD_RES	1	1
FT	ACT_SITE	10	10
FT	ACT_SITE	35	35
FT	ACT_SITE	104	104
FT	DISULFID	19	72
FT	DISULFID	34	82
FT	DISULFID	52	97
FT	DISULFID	94	111
SO	SEQUENCE	111 AA; 12461 MW; D64BA72456C10788	CRC64;

```

Query Match 45.8%; Score 264.5; DB 1; Length 111;
Best Local Similarity 42.7%; Pred. No. 1.5e-21;
Matches 47; Conservative 19; Mismatches 37; Indels 7; Gaps 2

QY 2 DMLFPOKKHLNTRDVCNNIMSTLW.F---HCKDKNTFIYSRPPVPAICGIIASKNV 57
DB 2 NMAKFEKHICSTSIDCNTIMDKAIYIVGCKCRERNFIFLISEDNVATCGVSPDRE 61
QY 58 LTTSEFYISDC---NVTSPCKYKIKKSTNFCVTCENQAPVHEVGVHC 104
DB 62 LSTTSFKLNTCIRDSITPRPCPPHSPDNKKICVACXKCEKOLPVHFEVIGIKC 111

RESULT 5
RNP_IGUIG STANDARD; PRT; 119 AA.
ID RNP_IGUIG
AC P80287;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Ribonuclease pancreatic (EC 3.1.27.5) (Rnase 1) (Rnase A).
OS Iguana iguana (Common Iguana).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauvia; Squamata; Iguania; Iguanidae; Iguaninae; Iguana.
RX NCBI_TaxID=8517;
RN [1]
RP SEQUENCE.
RC TISSUE=Pancreas; PubMed=8307028;
RX Zhao W., Beintema J.J., Hofsteenge J.;
RT "The amino acid sequence of iguana (Iguana iguana) pancreatic
RT ribonuclease.";
RL Eur. J. Biochem. 219:641-646(1994).
-1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-
phosphates and 3'-cyclic phosphate intermediates.
CC with 2',3'-cyclic phosphate intermediates.
CC CC CC CC CC CC CC CC CC CC CC CC CC CC CC CC CC CC CC CC CC CC
-1- SUBCELLULAR LOCATION: Secreted.
CC CC CC CC CC CC CC CC CC CC CC CC CC CC CC CC CC CC CC CC CC CC
-1- TISSUE SPECIFICITY: PANCREAS.
DR HSP: P00656; ILSQ.
DR InterPro: IPR001427; RNaseA.
DR Pfam: PF00074; RNaseA.
DR PRINTS: PR00794; RIBONUCLEASE.
DR PRODOM: PD000535; RNaseA.
DR SMART: SM00092; RNase_Pc.1.
DR PROSITE: PS00127; RNASE_PANCREATIC; 1.
KW Hydrolase; Nuclease; Endonuclease.
FT MOD_RES 1
FT DISULFID 25 80
FT DISULFID 39 91
FT DISULFID 57 106
FT ACT_SITE 10 10
FT ACT_SITE 40 40
FT ACT_SITE 113 113
SQ SEQUENCE 119 AA; 13324 MW; 6072P5B7B15BD5A CRC64;

Query Match 25.0%; Score 144; DB 1; Length 119;
Best Local Similarity 30.1%; Pred. No. 1.1e-08;
Matches 34; Conservative 19; Mismatches 44; Indels 16; Gaps 5

QY 2 DMLFPOKKHLNTRDVCNNIMSTLW.F---STNLFHCKDKNTFIYSRPPVPAIC--KG 50
DB 2 DMSRQNNKHIDYPEFSASNPNAYCDLMMQORLNLNTKCKTRNTFYHASELSLEQVCGSG 61
QY 51 ITASKNVLTSTSE-FYISDC---NVTSPCKYKIKKSTNFCVTCENQAPVHVF 98
DB 62 THEEDNLXDSNESFDLTDCKKNVGYTAPSSCKYNGTPTGTRIRIACENNQPVHF 114

RESULT 6
RNP_GALMU STANDARD; PRT; 124 AA.
ID RNP_GALMU

```

```

AC P00680;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Ribonuclease pancreatic (EC 3.1.27.5) (RNase 1) (RNase A).
GN RNASE1 OR RN51.
OS Galesa musteloides (Culis).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriocognathi; Cavillidae; Galesa.
OX NCBI_TaxID=10146;
RN [1]
RP MEDLINE=87036770; PubMed=6571219;
RX Beutema J.J., Neuteboom B.;
RA "Origin of the duplicated ribonuclease gene in guinea-pig: comparison
RT of the amino acid sequences with those of two close relatives:
RT capybara and culs ribonuclease.";
RL J. Mol. Evol. 19:145-152(1983).
CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-
CC phosphates and 3'-phosphooligonucleotides ending in C-P or U-P
CC with 2',3'-cyclic phosphate intermediates.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: PANCREAS.
CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
DR PIR: A00827; NRUI.
DR HSSP: P00656; ISRN.
DR InterPro: IPR001427; RNaseA.
DR Pfam: PF00074; RNaseA; 1.
DR PRINTS: PR00794; RIBONUCLEASE.
DR ProDom: PD000535; RNaseA; 1.
DR SMART: SM00092; RNase_Pc; 1.
DR PROSITE: PS00127; RNASE_PANCREATIC; 1.
DR KEGG: K00001; RNaseA.
KW Hydrolyase; Nuclease; Endonuclease.
FT DISULFID 26 84 BY SIMILARITY.
FT DISULFID 40 95 BY SIMILARITY.
FT DISULFID 58 110 BY SIMILARITY.
FT DISULFID 65 72 BY SIMILARITY.
FT ACT_SITE 12 12 BY SIMILARITY.
FT ACT_SITE 41 41 BY SIMILARITY.
FT ACT_SITE 119 119 BY SIMILARITY.
FT VARIANT 1 1 MISSING (IN 1/3 OF THE MOLECULES).
SQ SEQUENCE 124 AA; 13870 MW; 609C7E251A7BBA25 CRC64;

Query Match 22.9%; Score 132; DB 1; Length 124;
Best Local Similarity 30.6%; Pred. No. 2.3e-07;
Matches 38; Conservative 18; Mismatches 36; Indels 32; Gaps 7;

OY 1 SDMLTFQKKHL-----TNRDVCNNIM---STNLFHCKDKNTFTISREPPYKATCKG 50
DB 3 SSAMKFORQHMDSQCHPDTNTN--YCNEWVRSMTOGRCKRPVNTFVHEPLEAVQAVC-- 58
OY 51 IIAKKNV-----LTTSEFYLDPCNVTSRP---CKYKLRKSTNTFCVTGEN--QA 94
DB 59 --SQKNVCKNGQTCNGYSHSSMRTDCRVTSSSKYPCSTRMQAKSITIVACEGTPTV 116
OY 95 PVHF 98
DB 117 PVHF 120

RESULT 7
ANGL_MOUSE STANDARD; PRT; 145 AA.
AC O64438;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Angiogenin-related protein precursor.
GN ANGRP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;

```

```

RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129; TISSUE=Liver;
RX MEDLINE=96079109; PubMed=8530072;
RA Brown W.E., Noble V., Subramanian V., Shapiro R.;
RT "The mouse angiogenin gene family: structures of an angiogenin-related
RT protein gene and two pseudogenes.";
RL Genomics 29:200-206(1995).
CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: U22519; AAA91367.1; -.
DR HSSP: P03950; 1AAV.
DR MGP: MGI:104984; Angpr.
DR InterPro: IPR001427; RNaseA.
DR Pfam: PF00074; RNaseA; 1.
DR PRINTS: PR00794; RIBONUCLEASE.
DR ProDom: PD000535; RNaseA; 1.
DR SMART: SM00092; RNase_Pc; 1.
DR PROSITE: PS00127; RNASE_PANCREATIC; 1.
KW Signal; Hydrolyase; Nuclease; Endonuclease.
FT SIGNAL 1 24
FT CHAIN 25 145 ANGIOGENIN-RELATED PROTEIN.
FT MOD_RES 25 25 PYROLIDONE CARBOXYLIC ACID (BY
FT SIMILARITY).
FT ACT_SITE 37 37 BY SIMILARITY.
FT ACT_SITE 64 64 BY SIMILARITY.
FT ACT_SITE 137 137 BY SIMILARITY.
FT DISULFID 50 104 BY SIMILARITY.
FT DISULFID 63 115 BY SIMILARITY.
FT DISULFID 81 130 BY SIMILARITY.
SQ SEQUENCE 145 AA; 16612 MW; 29A6EB814429C4AD CRC64;

Query Match 22.6%; Score 130.5; DB 1; Length 145;
Best Local Similarity 38.2%; Pred. No. 3.9e-07;
Matches 29; Conservative 11; Mismatches 29; Indels 7; Gaps 3;

OY 30 CKDNKTFYSREPPYKATC--KGIASKNV-LTTSEFYLDPCNVTSR---PCKYKLRKS 82
DB 63 CKDVNTFPHDKNNIKAIKCKGSPYGRNLAIKSRFOYTTCTYKGRSPRPCKYRASKG 122
OY 83 TNEFCVTCENQAPVHF 98
DB 123 FRYIIIGCENGMPVHF 138

RESULT 8
ANGL_CERAE STANDARD; PRT; 146 AA.
AC O8WN66;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Angiogenin precursor (EC 3.1.27.-) (Ribonuclease 5) (RNase 5).
GN ANG OR RNASE5.
OS Cercopithecus aethiops (Green monkey) (Griwet).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheinae; Cercopithecus;
OX NCBI_TaxID=9534;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21918422; PubMed=11919285;
RA Zhang J., Rosenberg H.F.;
RT "Diversifying selection of the tumor-growth promoter angiogenin in
RT primate evolution.";

```

Query Match	22.2%	Score 128:	DB 1;	Length 148:
Best Local Similarity	34.0%;	Pred. No.	7.3e-07;	

[illegible]

```
Query Match          21.8%   Score 126; DB_1; Length 120;  
Best Local Similarity    29.9%; Pred.No.1e-06;  
Matches      35; Conservative     18; Mismatches       36; Indels    28; Gaps        7
```

OY 6 FOKKHL-----TNTRDVDCNNIM-STNLF--CKRKDNPFYSRPEPKAICGIIASKVV 57
 |::|::| ||::| ||::|::| |:
Db 8 FERQHMDRGSSSTPNPNCNEEMKRNRMTQGCKACKVFNVTFHEPLADVAQVC---FQRKV 63

OY 58 L-----TTSEFYFLSDCWNVTSRP----CKYLKKSTNFECYCENQ--APVHF 98
 |::|::| ||
Db 64 LCKNQGTNCYCNSNMHITTCDKRVTSNDSPNPNCSTYTSDEBKSIIVACGEONPIVPVHF 120

RESULT 11
RNP_BALAC

ID	RNP_BALAC	STANDARD:	PRT:	124 AA.
AC	P00673;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Ribonuclease pancreatic (EC 3.1.27.5) (Rnase 1) (Rnase A).			
GN	RNASE1 OR RN51.			
OS	Balaenoptera acutorostrata (Minke whale) (lesser rorqual).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Cetacea; Mysticeti;			
OX	Balaenopteridae; Balaenoptera.			
RN	NCBI_TaxID=9767;			
[1]				
RP	SEQUENCE.			
RX	MEDLINE=76277855; PubMed=962870;			
RA	Emmens M., Welling G.W., Beintema J.J.;			
RT	"The amino acid sequence of pike-whale (lesser-rorqual) pancreatic			
RL	ribonuclease.";			
CC	Biochem. J. 157:317-323(1976).			
CC	-1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-			
CC	phosphates and 3'-phosphooligonucleotides, ending in C-P or U-P			
CC	with 2',3'-cyclic phosphate intermediates.			
CC	-1- SUBCELLULAR LOCATION: Secreted.			
CC	-1- TISSUE SPECIFICITY: PANCREAS.			
CC	-1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.			
DR	PIR: A00818; NMRKX.			
DR	HSP: P00656; ISRN.			
DR	InterPro: IPR01427; RNaseA.			
DR	pfam: PF00074; rnasea: 1.			
DR	PRINTS: PR00794; RIBONUCLEASE.			
DR	ProDom: PD000535; RNaseA: 1.			
DR	SMART: SM00092; RNase_Pc: 1.			
KM	PROSITE: PS00127; RNASE_PANCREATIC; 1.			
KW	Hydrolase; Nuclease; Endonuclease; Glycoprotein.			
FT	DISULFID 26 BY SIMILARITY.			
FT	DISULFID 40 95 BY SIMILARITY.			
FT	DISULFID 58 110 BY SIMILARITY.			
FT	DISULFID 65 72 BY SIMILARITY.			
FT	ACT_SITE 12 12 BY SIMILARITY.			
FT	ACT_SITE 41 41 BY SIMILARITY.			
FT	ACT_SITE 119 119 BY SIMILARITY.			
FT	CARBOHYD 76 N-LINKED (GLCNAC. . .); IN 30% OF THE			
SQ	SEQUENCE 124 AA: 14125 MW; F57475459F697E20 CRC64;			
	Query Match 21.7%; Score 125; DB 1; Length 124;			
	Best Local Similarity 28.6%; Pred. No. 1.3e+06;			
	Matches 34; Conservative 15; Mismatches 42; Indels 28; Gaps 6;			
OY	4 LTFQKHLLTNRDVD-----CNIATSNLF---HCKDKNFITYSRPEPKAIICKGIASK 55			
DB	6 MKFOROHMDSGNSGNNPNNYCOMMKRRKKTGRCKPVPFHESLDDPVKAVC----SOK 61			
OY	56 NVL-----TTSSEFLSDCAVTSNR-----CKYKLKSTNFCVTCENQ--APVHF 98			
DB	62 NVLKNGRTNCTYESNSTWHITDCRKQTGS SKIPCAVKTSSOKEKHIIIVACEGPPYPVHF 120			
	RESULT 12			
	ANGI_MACMU			
ID	ANGI_MACMU STANDARD: PRT: 146 AA.			
AC	O8WN63;			
DT	15-JUN-2002 (Rel. 41, Created)			
DT	15-JUN-2002 (Rel. 41, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Angiotensin precursor (EC 3.1.27.-) (Ribonuclease 5) (Rnase 5).			
GN	ANG OR RNASE5.			
OS	Macaca mulatta (Rhesus macaque).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;			
OX	Cercopithecinae; Macaca.			
RN	NCBI_TaxID=9544;			
[1]				

```

Query Match          21.7%; Score 125; DB 1; Length 124;
Best Local Similarity 28.6%; Pred. No. 1.3e-06;
Matches 34; Conservative 15; Mismatches 42; Indels 28; Gaps 6;

OY 4 LTFQKHLTLTRDYPD-----CNNIMSTNLTF--HCKDKMFYSRPPVPAICKGIASK 55
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 6 MKPQRQIHDSNSPGNNPNPNYCNQMMMRKMTQGGCKRPVNTFVHSLDLYAVAC-----SK 61
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

OY 56 NVL-----TTSSEFYLSDCNVTSPR-----CKYLLKSTNFTCYTCENQ--APVHF 98
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 62 NVLCKNGKRTNCEESNSTWHTIDCRQOTGSSSKYPNCAYKTSQEKHHIIVACEGNPVVPHF 120
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 12
ANGI_MACMU
ID ANGI_MACMU STANDARD; PRT; 146 AA.
AC O8BNM63:

DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Angiogenin precursor (EC 3.1.27.-) (Ribonuclease 5) (Rnase 5).
GN
GN OR RNASE5.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]

```

RP SEQUENCE FROM N.A.
 RA MEDLINE=21918422; PubMed=11919285;
 RT "Diversifying selection of the tumor-growth promoter angiogenin in
 RT primate evolution.";
 RL Mol. Biol. Evol. 19:438-445(2002).
 CC -1- FUNCTION: MAY FUNCTION AS A tRNA-SPECIFIC RIBONUCLEASE THAT BINDS
 CC TO ACTIN ON THE SURFACE OF ENDOTHELIAL CELLS; ONCE BOUND,
 CC ANGIOGENIN IS ENDOCYTOSED AND TRANSLOCATED TO THE NUCLEUS, THEREBY
 CC PROMOTING THE ENDOTHELIAL INVASIVENESS NECESSARY FOR BLOOD VESSEL
 CC FORMATION. ANGIOGENIN INDUCES VASCULARIZATION OF NORMAL AND
 CC MALIGNANT TISSUES. ABOLISHES PROTEIN SYNTHESIS BY SPECIFICALLY
 CC HYDROLYZING CELLULAR TRNAs (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AF41657; A161649.1;
 KM Hydrolyase; Nuclease; Endonuclease; Angiogenesis;
 FT SIGNAL 1 24
 FT CHAIN 1 146
 FT MOD_RRS 25 146
 FT ACT_SITE 37 37 BY SIMILARITY.
 FT ACT_SITE 64 64 BY SIMILARITY.
 FT ACT_SITE 138 138 BY SIMILARITY.
 FT DISULFID 50 105 BY SIMILARITY.
 FT DISULFID 63 116 BY SIMILARITY.
 FT DISULFID 81 131 BY SIMILARITY.
 SQ SEQUENCE 146 AA; 16301 MW; E39A89215DB2A244 CRC64;
 Query Match 21.1%; Score 121.5; DB 1; Length 146;
 Best Local Similarity 28.7%; Pred. No. 3.5e-06;
 Matches 29; Conservative 17; Mismatches 32; Indels 23; Gaps 4;
 QY 5 TPYKHLTNTRDVDCNNIMSTNLFHCKDKNTFYSRPEPKAIC---KGIISKNV-LTT 60
 Db 53 TMRRHFLSP-----CKDITFVHGNNHHITAIICDGDNGSPYGGNLKIST 97
 QY 61 SEFYLSDCNVTST---RPEYKYLKSTNTPFCVTCENAPYH 97
 Db 98 SFPOVTFCKLRGSGPRPCOYRATRGSRNIVGCEGLPYH 138
 RESULT 13
 RNP_CAVPO STANDARD; PRT; 128 AA.
 ID RNP_CAVPO
 AC P06679;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Ribonuclease pancreatic B (EC 3.1.27.5) (Rnase IB).
 OS Cavia porcellus (Guinea pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Hystriocognathi; Cavidae; Cavia.
 OX NCBI_TaxID=10141;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Pancreas;
 RX MEDLINE=77185023; PubMed=862624;
 RA van den Berg A., van den Hende-Timmer L., Hofsteenge J., Gastra W.,
 RA Beutema J.J.;
 RT "Guinea-pig pancreatic ribonucleases. Isolation, properties, primary
 RT structure and glycosylation."
 RL Eur. J. Biochem. 75:91-100(1977).

CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-
 CC phosphates and 3'-phosphooligonucleotides ending in C-P or U-P
 CC with 2',3'-cyclic phosphate intermediates.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: PANCREAS.
 CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
 CC -----
 DR PIR; A00826; NRGPB.
 DR HSSP; P00656; ISRN.
 DR InterPro: IPR001427; RnaseA.
 DR Pfam: PF00794; RnaseA.1.
 DR PRINTS; PR00794; RIBONUCLEASE.
 DR PRODOM; PD000535; RnaseA; 1.
 DR SMART; SM00092; Rnase_Pc; 1.
 DR PROSITE; PS00127; Rnase_PANCREATIC; 1.
 KM Hydrolyase; Nuclease; Endonuclease; glycoprotein.
 FT DISULFID 26 84 BY SIMILARITY.
 FT DISULFID 40 95 BY SIMILARITY.
 FT DISULFID 58 110 BY SIMILARITY.
 FT DISULFID 65 72 BY SIMILARITY.
 FT ACT_SITE 12 12 BY SIMILARITY.
 FT ACT_SITE 41 41 BY SIMILARITY.
 FT ACT_SITE 119 119 BY SIMILARITY.
 FT CARBOHYD 21 21 N-LINKED (GLCNAC. . .).
 FT CARBOHYD 34 34 N-LINKED (GLCNAC. . .).
 FT VARIANT 64 64 L->P.
 SQ SEQUENCE 128 AA; 14406 MW; A2F4101A1A33E93B CRC64;
 Query Match 20.8%; Score 120; DB 1; Length 128;
 Best Local Similarity 28.3%; Pred. No. 4.4e-06;
 Matches 35; Conservative 21; Mismatches 37; Indels 30; Gaps 7;
 QY 1 SDWTFPKKHL-----TNTRDVDCNNIM---STNLFHCKDKNTFYSRPEPKAICGKI 51
 Db 3 SSAMKPRQIMDPGSSNSNT-CNVMMIRNNTGRCRKFVNTFVIESLADQAVC--- 58
 QY 52 IASKNVL-----TSEFYLSDCNVTST---RPEYKYLKSTNTPFCVTCENQ--AP 95
 Db 59 -FQKNVLCKNQTCNOCYSYRMRITDCRVSSSKFPCSYRMSQAKSIVACEGDYYP 117
 QY 96 VHF 98
 Db 118 VHF 120
 RESULT 14
 RNP_PROGU STANDARD; PRT; 128 AA.
 ID RNP_PROGU
 AC P04059;
 DT 01-NOV-1986 (Rel. 03, Created)
 DT 01-NOV-1986 (Rel. 03, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Ribonuclease pancreatic (EC 3.1.27.5) (Rnase I) (Rnase A).
 GN RNAS1 OR RN1.
 OS Proechimys guairae (Castiagua).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Hystriocognathi; Echimyidae; Proechimys.
 OX NCBI_TaxID=10163;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Pancreas;
 RX MEDLINE=83000399; PubMed=7115727;
 RA Beutema J.J., Knol G., Martena B.;
 RT "The primary structures of pancreatic ribonucleases from African
 RT porcupine and castiagua, two hystriocomorph rodent species."
 RL Biochim. Biophys. Acta 705:102-110(1982).
 CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-
 CC phosphates and 3'-phosphooligonucleotides ending in C-P or U-P
 CC with 2',3'-cyclic phosphate intermediates.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: PANCREAS.
 CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
 DR PIR; A00821; NRKS.
 DR HSSP; P00656; ISRN.

```

DR InterPro: IPR001427; RNaseA.
DR Pfam: PF00074; RNaseA; 1.
DR PRINTS: PR00794; RIBONUCLEASE.
DR ProDom: PD000535; RNaseA; 1.
DR SMART: SM00092; RNaseA; 1.
DR PROSITE: PS00127; RNASE_PANCREATIC; 1.
KW Hydrolase; Nuclease; Endonuclease; Glycoprotein.
FT DISULFID 26 84 BY SIMILARITY.
FT DISULFID 40 95 BY SIMILARITY.
FT DISULFID 58 110 BY SIMILARITY.
FT DISULFID 65 112 BY SIMILARITY.
FT ACT_SITE 12 12 BY SIMILARITY.
FT ACT_SITE 41 41 BY SIMILARITY.
FT ACT_SITE 119 119 BY SIMILARITY.
FT CARBOHYD 34 34 N-LINKED (GLCNAC...).
SQ SEQUENCE 128 AA: 14244 MW: 2DBS8093A9D3C936 CRC64;

Query Match 20.8%; Score 120; DB 1; Length 128;
Best Local Similarity 29.9%; Pred. No. 4; 4e-06;
Matches 35; Conservative 18; Mismatches 36; Indels 28; Gaps 7;

QY 6 FOKKHL-----TTRVDCCNINM-STNLF--HCKDKNTFYSPREPVKAIKGIASKNV 57
DB 8 FOKHIDSSGSPSTNPVNCNAMKSRNMTQERCKPVTFVHEPLADVQAVC-----FOKNV 63
QY 58 -----LTFSEFYLSDCNVTSR-----PCCKYKLLKSTNTEVCYCENQ--APVHF 98
DB 64 PCKNGSNCYEISNMHITDCRLTNSKRPDCVLTFRTOSEKSLTVACENPPYVPHF 120

RESULT 15
ANGI_MOUSE STANDARD: PRT: 145 AA.
AC P21570:
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Angiogenin precursor (EC 3.1.27.-).
GN ANG.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91025023; PubMed=2222458;
RA Bond M.D., Vallee B.L.;
RT "Isolation and sequencing of mouse angiogenin DNA.";
RL Biochem. Biophys. Res. Commun. 171:988-995(1990).
[2]
RP PARTIAL SEQUENCE.
RC TISSUE-Serum;
RX MEDLINE=93192291; PubMed=8448182;
RA Bond M.D., Strieter D.J., Vallee B.L.;
RT "Characterization and sequencing of rabbit, pig and mouse
RT angiogenins: discernment of functionally important residues and
RT regions.";
RL Biochim. Biophys. Acta 1162:177-186(1993).
CC -!- FUNCTION: MAY FUNCTION AS A TRNA-SPECIFIC RIBONUCLEASE THAT BINDS
CC TO ACTIN ON THE SURFACE OF ENDOTHELIAL CELLS; ONCE BOUND,
CC ANGIOGENIN IS ENDOCYTOSED AND TRANSLOCATED TO THE NUCLEUS, THEREBY
CC PROMOTING THE ENDOTHELIAL INVASIVENESS NECESSARY FOR BLOOD VESSEL
CC FORMATION. ANGIOGENIN INDUCES VASCULARIZATION OF NORMAL AND
CC MALIGNANT TISSUES. ABOLISHES PROTEIN SYNTHESIS BY SPECIFICALLY
CC HYDROLYZING CELLULAR TRNAs.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial

```

```

CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U22516; AAA91366.1; -.
DR PIR: A35932; A35932.
DR HSSP: P03950; 1A4Y.
DR MGD: MGI:88022; Ang.
DR InterPro: IPR001427; RNaseA.
DR Pfam: PF00074; RNaseA; 1.
DR PRINTS: PR00794; RIBONUCLEASE.
DR ProDom: PD000535; RNaseA; 1.
DR SMART: SM00092; RNaseA; 1.
DR PROSITE: PS00127; RNASE_PANCREATIC; 1.
KW Hydrolase; Nuclease; Endonuclease; Angiogenesis;
KW Protein synthesis inhibitor; Signal.
FT CHAIN 1 24
FT SIGNAL 1 24
FT MOD_RES 25 25
FT ACT_SITE 37 37 BY SIMILARITY.
FT ACT_SITE 64 64 BY SIMILARITY.
FT ACT_SITE 137 137 BY SIMILARITY.
FT DISULFID 50 104 BY SIMILARITY.
FT DISULFID 63 115 BY SIMILARITY.
FT DISULFID 81 130 BY SIMILARITY.
SQ SEQUENCE 145 AA: 16228 MW: 06944260B8764938 CRC64;

Query Match 20.7%; Score 119.5; DB 1; Length 145;
Best Local Similarity 30.8%; Pred. No. 5; 7e-06;
Matches 33; Conservative 12; Mismatches 45; Indels 17; Gaps 5;

QY 9 KHLTNRDVID-----CNIMSTNLF--HCKDKNTFYSPREPVKAIKGIASKNV 56
DB 32 KFLTQHDAKPKGRDORCERMKRSLSPCKDVTFTFGKSNIKAIKGNAGSPYREN 91
QY 57 V-LTFSEFYLSDCNVTSR-----RCKYKLLKSTNTEVCYCENQAPVHF 98
DB 92 LKMSKSPFOVTKHTGSGSPRPPCOYRASAGFRHVIVACENGLPVHF 138

```

Search completed: June 25, 2003, 14:50:04
Job time : 6.40155 secs